



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Boyle, William J.
- (ii) TITLE OF INVENTION: Osteoprotegerin Binding Proteins
- (iii) NUMBER OF SEQUENCES: 39
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Amgen Inc.
 - (B) STREET: One Amgen Center Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Winter, Robert B.
 - (C) REFERENCE/DOCKET NUMBER: A-451G

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Pro Asn Arg Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT

52

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA

37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Asn Ala Gly Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTTGATTCT AGAAGGAGGA ATAACATATG CATGAAAACG CAGGTCTGCA G

51

B1
Cont.

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATCCGCGGA TCCTCGAGTT AGTCTATGTC CTGAACTTTG AA

42

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Asp Thr Leu Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTGATTCT AGAAGGAGGA ATAACATATG TCTGAAGACA CTCTGCCGGA CTCC

54

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

B1
Cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Gln Ala Phe Gln Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTTGATTCT AGAAGGAGGA ATAACATATG AAACAAGCTT TTCAGGGG

48

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Glu Leu Gln His Gln Asp Ile Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTTGATTCT AGAAGGAGGA ATAACATATG AAAGAACTGC AGCACATTGT G

51

31
Cont.

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Phe Ser Gly Gln Asp Ile Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTGTATTCT AGAAGGAGGA ATAACATATG CAGCGTTTCT CTGGTGCTCC A

51

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Glu Gly Ser Trp Gln Asp Ile Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

B1
Cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTCTCCTCA TATGGAAGGT TCTTGTTGG ATGTGGCCCA

40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Arg Gly Lys Pro Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTCTCCTCA TATGCGTGGT AAACCTGAAG CTCAACCATT TGCA

44

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Lys Pro Glu Ala Gln Asp Ile Asp
1 5

B1
Cont.

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT

53

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met His Leu Thr Ile Gln Asp Ile Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCATCGGGT TCCCATAAAG

60

TCACT

65

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

B1
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Ile Asn Ala Gln Asp Ile Asp
1 5

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT

59

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Lys Pro Glu Ala Gln Pro Phe Ala His
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCTAGGCC TGTACTTTTCG AGCGCAGATG

30

B!
cont.

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTCTCTCGA GTGGACAACC CAGAAGCCTG AGGCCAGCC ATTTGC

46

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

B1
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTTCCACC ATGAACAAGT GGCTGTGCTG CGCACTCCTG GTGCTCCTGG ACATCA

56

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGATGATGT CCAGGAGCAC CAGGAGTGCG CAGCACAGCC ACTTGTCAT GGTGGA

56

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser
1				5					10					15	
Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser					
			20					25							

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser
1				5					10					15	
Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Cys				
			20					25							

31
cont.

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
 1 5 10 15
 Met

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
 1 5 10 15
 Met Cys

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 158..1105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCTCGGAT CCACTACTCG ACCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG 60
 CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA 120

B1
Cont.

TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC																ATG CGC CGG GCC AGC CGA	175
																Met Arg Arg Ala Ser Arg	
																1	5
GAC	TAC	GGC	AAG	TAC	CTG	CGC	AGC	TCG	GAG	GAG	ATG	GGC	AGC	GGC	CCC	223	
Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu	Glu	Met	Gly	Ser	Gly	Pro		
			10				15				20						
GGC	GTC	CCA	CAC	GAG	GGT	CCG	CTG	CAC	CCC	GCG	CCT	TCT	GCA	CCG	GCT	271	
Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro	Ala	Pro	Ser	Ala	Pro	Ala		
			25				30				35						
CCG	GCG	CCG	CCA	CCC	GCC	GCC	TCC	CGC	TCC	ATG	TTC	CTG	GCC	CTC	CTG	319	
Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	Phe	Leu	Ala	Leu	Leu		
			40				45				50						
GGG	CTG	GGA	CTG	GGC	CAG	GTG	GTC	TGC	AGC	ATC	GCT	CTG	TTC	CTG	TAC	367	
Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Ile	Ala	Leu	Phe	Leu	Tyr		
			55				60				65				70		
TTT	CGA	GCG	CAG	ATG	GAT	CCT	AAC	AGA	ATA	TCA	GAA	GAC	AGC	ACT	CAC	415	
Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	His		
			75				80				85						
TGC	TTT	TAT	AGA	ATC	CTG	AGA	CTC	CAT	GAA	AAC	GCA	GGT	TTG	CAG	GAC	463	
Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Gly	Leu	Gln	Asp		
			90				95				100						
TCG	ACT	CTG	GAG	AGT	GAA	GAC	ACA	CTA	CCT	GAC	TCC	TGC	AGG	AGG	ATG	511	
Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Cys	Arg	Arg	Met		
			105				110				115						
AAA	CAA	GCC	TTT	CAG	GGG	GCC	GTG	CAG	AAG	GAA	CTG	CAA	CAC	ATT	GTG	559	
Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	Val		
			120				125				130						
GGG	CCA	CAG	CGC	TTC	TCA	GGA	GCT	CCA	GCT	ATG	ATG	GAA	GGC	TCA	TGG	607	
Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	Trp		
			135				140				145				150		
TTG	GAT	GTG	GCC	CAG	CGA	GGC	AAG	CCT	GAG	GCC	CAG	CCA	TTT	GCA	CAC	655	
Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	His		
			155				160				165						
CTC	ACC	ATC	AAT	GCT	GCC	AGC	ATC	CCA	TCG	GGT	TCC	CAT	AAA	GTC	ACT	703	
Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr		
			170				175				180						
CTG	TCC	TCT	TGG	TAC	CAC	GAT	CGA	GGC	TGG	GCC	AAG	ATC	TCT	AAC	ATG	751	
Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met		
			185				190				195						
ACG	TTA	AGC	AAC	GGA	AAA	CTA	AGG	GTT	AAC	CAA	GAT	GGC	TTC	TAT	TAC	799	
Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr		
			200				205				210						
CTG	TAC	GCC	AAC	ATT	TGC	TTT	CGG	CAT	CAT	GAA	ACA	TCG					

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn 250 255 260	943
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly 265 270 275	991
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn 280 285 290	1039
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 295 300 305 310	1087
AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG Lys Val Gln Asp Ile Asp 315	1135
ATGTCCTAGA TGT'TTGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT	1195
ACTAAGAGAC ATGGCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG	1255
GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT	1315
ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT	1375
GA AAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA	1435
TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG	1495
TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT	1555
TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTTACAG	1615
GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA	1675
AATATTTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA	1735
ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT	1795
CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAAC TTAATAGAGT CTTCAGACTT	1855
GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAAATAAAA TGAATACCTT GAATAATAAG	1915
TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC	1975
ATAGCCAAAA AGGATACATA ATAGGCTACT GAAATCTGTC AGGAGTATTT ATGCAATTAT	2035
TGAACAGGTG TCTTTTTTTT CAAGAGCTAC AAATTGTAAA TTTTGTTTCT TTTTTTTCCC	2095
ATAGAAAATG TACTATAGTT TATCAGCCAA AAAACAATCC ACTTTTAAAT TTAGTGAAAG	2155
TTATTTTATT ATACTGTACA ATAAAAGCAT TGTCTCTGAA TGTTAATTTT TTGGTACAAA	2215
AAATAAATTT GTACGAAAAC CTGAAAAAAA AAAAAAAAAA AAAAAAAGG GCGGCCGCTC	2275
TAGAGGGCCC TATTCTATAG	2295

B
cont.

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15
 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110
 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285

B1
 cont

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
305 310 315

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 185..1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGCTTGGTA CCGAGCTCGG ATCCACTACT CGACCCACGC GTCCGCGCGC CCCAGGAGCC 60
 AAAGCCGGGC TCCAAGTCGG CGCCCCACGT CGAGGCTCCG CCGCAGCCTC CGGAGTTGGC 120
 CGCAGACAAG AAGGGGAGGG AGCGGGAGAG GGAGGAGAGC TCCGAAGCGA GAGGGCCGAG 180
 CGCC ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG 229
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
 1 5 10 15
 GAG GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC 277
 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
 20 25 30
 GCC CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC GCC TCC CGC TCC 325
 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 ATG TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC 373
 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 GTC GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA 421
 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75
 TCA GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA 469
 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
 80 85 90 95
 AAT GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA 517
 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
 100 105 110
 ATA CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG 565
 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
 115 120 125

B1
Cont.

CAA AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu 130 135 140	613
AAA GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys 145 150 155	661
CTT GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile 160 165 170 175	709
CCA TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg 180 185 190	757
GGT TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile 195 200 205	805
GTT AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg 210 215 220	853
CAT CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met 225 230 235	901
GTG TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu 240 245 250 255	949
ATG AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His 260 265 270	997
TTT TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu 275 280 285	1045
GAA ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln 290 295 300	1093
GAT GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 305 310 315	1135
TGAGCCCCAG TTTTGGAGT GTTATGTATT TCCTGGATGT TTGGAAACAT TTTTAAAC	1195
AAGCCAAGAA AGATGTATAT AGGTGTGTGA GACTACTAAG AGGCATGGCC CCAACGGTAC	1255
ACGACTCAGT ATCCATGCTC TTGACCTTGT AGAGAACACG CGTATTTACA GCCAGTGGGA	1315
GATGTTAGAC TCATGGTGTG TTACACAATG GTTTTTTAAAT TTTGTAATGA ATTCCTAGAA	1375
TTAAACCAGA TTGGAGCAAT TACGGGTGTA CCTTATGAGA AACTGCATGT GGGCTATGGG	1435
AGGGGTTGGT CCCTGGTCAT GTGCCCCTTC GCAGCTGAAG TGGAGAGGGT GTCATCTAGC	1495
GCAATTGAAG GATCATCTGA AGGGGCAAAT TCTTTTGAAT TGTTACATCA TGCTGGAACC	1555
TGCAAAAAAT ACTTTTTCTA ATGAGGAGAG AAAATATATG TATTTTTATA TAATATCTAA	1615

81
cont.

AGTTATATTT CAGATGTAAT GTTTTCTTTG CAAAGTATTG TAAATTATAT TTGTGCTATA 1675
 GTATTTGATT CAAAATATTT AAAAATGTCT TGCTGTTGAC ATATTTAATG TTTTAAATGT 1735
 ACAGACATAT TTAAC TGGTG CACTTTGTAA ATTCCCTGGG GAAAACTTGC AGCTAAGGAG 1795
 GGGAAAAAAA TGTGTGTTTCC TAATATCAAA TGCAGTATAT TTCTTCGTTC TTTTAAAGTT 1855
 AATAGATTTT TTCAGACTTG TCAAGCCTGT GCAAAAAAAT TAAATGGAT GCCTTGAATA 1915
 ATAAGCAGGA TGTGCGCCAC CAGGTGCCTT TCAAATTTAG AAATAATTG ACTTTAGAAA 1975
 GCTGACATTG CAAAAAGGA TACATAATGG GCCACTGAAA TCTGTCAAGA GTAGTTATAT 2035
 AATTGTTGAA CAGGTGTTTT TCCACAAGTG CCGCAAATTG TACCTTTTTT TTTTTTTCAA 2095
 AATAGAAAAG TTATTAGTGG TTTATCAGCA AAAAAGTCCA ATTTTAATTT AGTAAATGTT 2155
 ATCTTATACT GTACAATAAA AACATTGCCT TTGAATGTTA ATTTTTTGGT AAAAAATAA 2215
 ATTTATATGA AAAAAAAA AAAAGGGCGG CCGCTCTAGA GGGCCCTATT CTATAGG 2272

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1 5 10 15
 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30
 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45
 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50 55 60
 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160

Bl
cont.

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

B¹
 cont